

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/071,338

CRF Processing Date: 3/19/2002

Edited by: A

Verified by: (STIC staff) 5/5/02

ENTERED

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APR 18 2002
TECH CENTER 1652/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING DATE: 03/19/2002
 PATENT APPLICATION: US/10/071,338 TIME: 18:47:50

Input Set : N:\Crf3\02272002\J071338.raw
 Output Set: N:\CRF3\03192002\J071338.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: SmithKline Beecham plc et al
 3 (ii) TITLE OF INVENTION: Novel compounds
 4 (iii) NUMBER OF SEQUENCES: 19
 5 (iv) CORRESPONDENCE ADDRESS:
 6 (A) ADDRESSEE: SmithKline Beecham
 7 (B) STREET: Two, New Horizons Court, Great West Road
 8 (C) CITY: Brentford
 9 (D) STATE:
 10 (E) COUNTRY: UK
 11 (F) ZIP: TW8 9EP

12 (v) COMPUTER READABLE FORM:

13 (A) MEDIUM TYPE: Diskette
 14 (B) COMPUTER: IBM Compatible
 15 (C) OPERATING SYSTEM: DOS
 16 (D) SOFTWARE: FastSEQ for Windows Version 2.0

17 (vi) CURRENT APPLICATION DATA:

C--> 18 (A) APPLICATION NUMBER: US/10/071,338
 C--> 19 (B) FILING DATE: 08-Feb-2002
 20 (C) CLASSIFICATION:

21 (vii) PRIOR APPLICATION DATA:

22 (A) APPLICATION NUMBER:
 23 (B) FILING DATE:

24 (viii) ATTORNEY/AGENT INFORMATION:

25 (A) NAME: Valentine, Jill B
 26 (B) REGISTRATION NUMBER:
 27 (C) REFERENCE/DOCKET NUMBER: P31731

28 (ix) TELECOMMUNICATION INFORMATION:

29 (A) TELEPHONE: 0181-9752000
 30 (B) TELEFAX: 0181-9756294
 31 (C) TELEX:

32 (2) INFORMATION FOR SEQ ID NO: 1:

33 (i) SEQUENCE CHARACTERISTICS:

34 (A) LENGTH: 7193 base pairs
 35 (B) TYPE: nucleic acid
 36 (C) STRANDEDNESS: single
 37 (D) TOPOLOGY: linear

38 (ii) MOLECULE TYPE: Other

39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40	CCATGGCGGG CGGCGGCTGC CCCGGAGCCT CGGCCGGACC GGTGACCAGG ACCACCCCGG	60
41	TGGGATAGTG GCCCGCCACC CGGCGCAGCA GACTCCCGGA CACGGACCCG TGGGTGTGCG	120
42	CGGAAAGGCC CGGAGGCCGG GTCACAGCCA CGGGTAACGC GCGGTGTCCT TGCCCGCGTA	180

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RAW SEQUENCE LISTING

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Input Set : N:\Crf3\02272002\J071338.raw

Output Set: N:\CRF3\03192002\J071338.raw

43	ATCGGGGTCC	AGATAGACGA	AGGCCCGGTG	GACGAGGAAG	TCCCGCACCT	CGTAGACCGT	240
44	GCACCAGCGC	CCGGCGGCC	ACTCGGGGTC	ACCCGCCCGC	CACGGCCCCG	CCCGGTGCTC	300
45	ACCGTGGGTG	GTGCCCTCCG	CGGCGAGGAG	TTCGGTCCCG	GTCAGAATCC	AGTTGACGGA	360
46	CCACAGATGG	TGGGTGATCG	AGCGGATGGT	GCCCCCGAGG	TCGTGGAAGA	GCCGGGCGAT	420
47	CTCGGACTTG	CCCCGGGCCA	GACCCCACTT	GGGGAAGAAG	AAGACCGCGT	CCTCGGCGAA	480
48	GTAGTCGATC	GCGGGGGTGC	CGTCGCTGCC	GACGCCGCCG	TTGTCGAACG	CCTTGAAGTA	540
49	CGCGGTGATG	ACCGCCTTGC	GCTGCTCGTC	CGTCATACCG	GCCGATGCCA	CGGACATGAA	600
50	ACGACCTCCA	GAGATTCCCG	GTGGCTGTGC	TGGGGCTGCG	GAAGGGGTGT	CCCCCGCGAA	660
51	GGACGGCGGA	CGCCGCGGAC	GCCGCGGCCG	TCTCCCCGGC	GGACGGGTCC	CAGCGTCTTG	720
52	GAGAGGGCTT	GGCGGCGGCT	TGACGCCGTG	CTGTCCCGCG	GCTTGCGGAA	CGCGAAGTAC	780
53	CGGCCAGCGT	ACGGGCGTTG	CACCGGACGT	GTACGCCGGT	CGGGACCCCT	CGTACCCCGC	840
54	GAGCCGGCCG	ACCCCGGCGG	CTCCGGGGGT	ACGGACGCGC	CGGACCGGCC	CGAGCCGACC	900
55	GGACGGGTCT	GACGGTGCGC	GTGGTTCCGG	TGTGTGCGAC	AGCTCGGACG	GACCGGACGG	960
56	TGCGCGTGGT	TCCGGTGTGT	CGGACAGCTC	GGACGGGTCT	GACGGTGCGC	GTGGTTCCGG	1020
57	CACGCCGGAC	GGGTCAATTG	CCGATCATGG	CGAGCAATGC	CGGGGTGTAC	CGTCCCCCGG	1080
58	ACACCGGGTG	GGAGATCGCG	GCCGTACACT	CCGCGAGGGA	CCGTCGTCC	AGCCGGATCG	1140
59	AGGCGGCGGC	GAGATTGTCC	GCGAGATGGG	CCGGGTTCGC	GGTGCCCGGG	ATCGGGACGA	1200
60	CGTCTCGCC	CCGGTGGTGC	AGCCAGGCGA	GCGCGAGCTG	TGCCAGGGTC	AGCCCCAGAC	1260
61	CGTCCGCGAC	CGGGCGCAGC	CGGTGCAGCA	ACGAGCGGTT	GCGCGCGAGG	GCCGGAGCGC	1320
62	TGAACCGGGG	CTGGCCCGCG	CGGAAGTCCT	CGTCCCCCAG	ATCGTCGGTG	GTGCGGATGG	1380
63	TGCCGGTGAG	AAAACCCCGT	CCCAGAGGGG	CGTAAGCGAC	GATCCCGATC	CCCAGTCCCC	1440
64	GGCAGACGGG	CACCACCTCG	TCCTCGATCC	CGCGCGACCA	CAGGCTCCAC	TCGCTCTGCA	1500
65	CCGCCGTCAC	CGGGTGACAC	GCGTCCGCCC	GGCGCAGCGT	GGCCGCGGAG	GGCTCGGAGA	1560
66	GACCGAGCCT	GCGGACCTTG	CCCTCGCGCA	CCAGCTCGGC	CACCGCACCC	ACGGTCTCCT	1620
67	CGATCGGCAC	CGCCGGGTCC	GTCCAGTGCT	GGTAGTACAG	GTGATGCGG	TCGGTGCCGA	1680
68	GACGACGCAG	GGACCGTTCT	CAGGCCGCGC	GGACGTAGGA	CGGCTCGCCG	CACAAGCCCT	1740
69	GGGAGGCGCC	GTCGGACGAG	CGCACCATGC	CGAACTTGGT	GGCGATCAGC	ACCTCGTCCC	1800
70	GGCGGCCCCG	GACCGCCCGT	CCGAGACGCT	CCTCACCGGC	GCCGAGCCCC	TGGACGTCCG	1860
71	CGGTGTCCAG	CAGGGTGACC	CCGGCGTCGA	CGGCGGCGCG	GATGGTGGCC	GTGCGCCGGG	1920
72	CGCGGTCCGG	GCGTCCGTAG	AAGTCGGTGG	TCGGCAGGCA	GCCGAGCCCC	TGGGCACTGA	1980
73	CCGGAAGGTC	CCGCAGGGCG	CGGACGGGCG	GACGCGGAAC	CGCGGCGGAC	ACGGAACCGG	2040
74	CCGGGGACTC	GGGCGGAGAG	CGGGACATAC	GGAACCTCCA	CAGGCGGAGC	CGGGAACGGG	2100
75	ACGAGGGCGA	GGACGGGACG	GAACGAAGGA	GAGGACGGGA	CGGACAGCAC	GGACGGGACG	2160
76	GACGGAACGG	AGTCGGGAAC	CGGGGGGGGT	GACCGGAACC	GGGCCGTCTT	TGGCCCTCCC	2220
77	CCGTCTCTCC	CGCCATCCGC	CGTTCTCCCC	CGTTCCCTCT	CCCGTCTCTC	AGCCAACACC	2280
78	GCCGCCCTTT	CCAAGCGCTT	GACACGGCAC	CGACAGCCGC	CGCCGGGCGC	CCGATGGGGA	2340
79	CCCGTGCCCG	CCGGTGAGCG	GCGGTGAGCG	CCGGTACGGG	ACCCACGCG	CCGCCGCCCG	2400
80	GGCGCCCGCC	AGGGCCCGCG	CGGCCACCCC	GGCCCGCCCC	GGCCGGAGCG	GCGATCCGGG	2460
81	CCGCTCGCTG	CAAGAGGAAC	ATCCACAGCC	GCACAAGGAG	CGCTCCGCAC	AGTGGGCACC	2520
82	ACGTCCGCCC	CGTCCCCCAC	ACCGTGGCCG	GTCCCCACCG	GACAGCACAG	CACCGCACAG	2580
83	CACCACATCG	CACGGCACAG	CACAGCACCA	CCGGCACGAG	GAACCAAGGA	AAGGAACCAC	2640
84	ACCACCATGA	CCTCAGTGGA	CTGCACCGCG	TACGGCCCCG	AGCTGCGCGC	GCTCGCCGCC	2700
85	CGGCTGCCCC	GGACCCCCCG	GGCCGACCTG	TACGCCTTCC	TGGACGCGCG	GCACACAGCC	2760
86	GCCGCCTCGC	TCCCCGGCGC	CCTCGCCACC	GCGCTGGACA	CCTTCAACGC	CGAGGGCAGC	2820
87	GAGGACGGCC	ATCTGCTGCT	GCGGCGCCTC	CCGGTGGAGG	CCGACGCCGA	CTCCCCCACC	2880
88	ACCCCGAGCA	GCACCCCGCG	GCCCAGGAGC	CGTCCCTGCG	TGACCATGGA	GGCCATGCTC	2940
89	GGACTGGTGG	GCCGCCGGCT	CGGTCTGCAC	ACGGGGTACC	GGGAGCTGCG	CTCGGGCACG	3000
90	GTCTACCACG	ACGTGTACCC	GTCGCCCCGG	GCGCACCAAC	TGTCCTCGGA	GACCTCCGAG	3060
91	ACGCTGCTGG	AGTTCCACAC	GGAGATGGCC	TACCACCGGC	TCCAGCCGAA	CTACGTCATG	3120

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Input Set : N:\Crif3\02272002\J071338.raw

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92	CTGGCCTGCT	CCCGGGCCGA	CCACGAGCGC	ACGGCGGCCA	CACTCGTCGC	CTCGGTCCGC	3180
93	AAGGCGCTGC	CCCTGTGGA	CGAGAGGACC	CGGGCCCGGC	TCCTCGACCG	GAGGATGCCC	3240
94	TGCTGCGTGG	ATGTGGCCTT	CCGCGGCGGG	GTGGACGACC	CGGGCGCCAT	CGCCAGGTC	3300
95	AAACCGCTCT	ACGGGGACGC	GGACGATCCC	TTCCTCGGGT	ACGACCGCGA	GCTGCTGGCG	3360
96	CCGGAGGACC	CCGCGGACAA	GGAGGCCGTC	GCCGCCCTGT	CCAAGGCGCT	CGACGAGGTC	3420
97	ACGGAGGCGG	TGTATCTGGA	GCCCCGCGAT	CTGCTGATCG	TCGACAACTT	CCGCACCACG	3480
98	CACGCGCGGA	CGCCGTTCTC	GCCCCGCTGG	GACGGGAAGG	ACCGCTGGCT	GCACCGCGTC	3540
99	TACATCCGCA	CCGACCGCAA	TGGACAGCTC	TCCGGCGGCG	AGCGCGCGGG	CGACGTCGTC	3600
100	GCCTTCACAC	CGCGCGGCTG	AGCTCCCGGG	TCCGACACCG	CGCGGCTGAA	CCCACGGTCC	3660
101	GGGGCCACG	GTCCGGCACC	GCGCGGCTGA	GGCCCCGGGT	CCGGCAGCGG	GCGGCTGAAC	3720
102	CCCCGCCCG	GGCCACCGCC	CGACCGCCCC	CGCGCACCGG	ACGCGCCCCG	CTGTACGGCG	3780
103	GTCCCGCCCG	GGCCCGTACA	CCTGAAGCGC	CCGGCGGACC	GCCGCCCCGC	CGGGGGACGG	3840
104	ACAGAGCCGG	GTGCGGGAGG	ACGTCTCTCC	GCACCCGGCT	CCCACCGTTC	CGCACCGACC	3900
105	GCACCCGACC	GTGCCCGCAG	CGCCACCGGC	ACCGCACCGC	CCGCGCCGGC	AGCCACCACA	3960
106	GGCGCCACG	CGCCCGCAG	GTGCCCGCGC	TGCTCAGCCC	CCGTCCACCG	GGCTGTCCAG	4020
107	GACCGCCCG	AGCGCGCCCC	CGATGAACTC	CCGGTCGGCG	GCCGACCCCC	CGGACCCCGC	4080
108	GAGATGCCCC	CACACTCCCC	GGATCACCTC	CAGCGAGGCA	TACGGCAGCA	GATCGGCCAC	4140
109	CCGCTTCTCG	TCCTCGACGG	CGAAACACAC	GTCCAGGGCG	CCGCGCAGCA	CCACGGCCCC	4200
110	CGCCGTGACG	GAGGCCAGCG	CGCCCTCGAC	GCTCCCCCCG	GCCCCGGGTG	TCGCCCCCAC	4260
111	ATCCGTGTTT	TCCCAGGTGC	GCACCATGGT	GAGCAGATCC	GCGGCGCCGG	GCCCGGAGAG	4320
112	GAAGACCTGC	TCCCAGAAGC	CGGTGAGGTA	CTCCTCGCGG	GTGGCGAAAC	CCAGCTCCCG	4380
113	GTGGGCACGG	CGGGCCCGAG	AGGAACCGCA	GGTCCCCCAC	CCGGCGAACA	CCCGGCCCGC	4440
114	CGCCTTCCGC	CCCCGCTCCC	CGGCGTCGGC	GCTGAGCGCC	GCGGCCAGAC	CGGACAGCAG	4500
115	GACCAGGCTG	TGCGGGCTGC	TCACCGGCGC	CCCGCAGATC	GGGGCGATCC	GGCGCACCAT	4560
116	CCCCGGATGC	GACACGGCCC	ACTGGTAGGC	GTGGGCCGCG	CCCATCGACC	AGCCCGTGAC	4620
117	CAGGGCCAGT	TCCCGTACCC	CCAGCTCCTC	GGTGAGCAGC	CGGTGCTGCG	CCGCGACATT	4680
118	GTCTGCGGA	GTGATCAGCG	GAAAGCGGGA	CCCCGACGGG	TGGTTGCCGG	GCGAGCTGGA	4740
119	GACCCCGTTG	CCGAAGAGTC	CGGCGGTGAC	GACGCAGTAC	CGCCGGGTGT	CCAGCGGCAG	4800
120	CCCCGACCCG	ATCAGCCAGT	CGTACCCGGT	GTGGTCCCGG	CCGAAGAACG	ACGGACAGAG	4860
121	CACCACGTTT	GTCCCGTCGG	CGTTCGGCGT	GCCGTACATG	GCGTAACCGA	TCCGGGCGTC	4920
122	CCGACGAGCC	TCCCGGTCCA	GCAACGGCAG	TTCGTGATC	TCGAATATGC	GGCATTCCAC	4980
123	CGTGACCTC	CTTGTTTCGAT	CCCCCGGAC	AACAGGTCGG	TCGTGGCCGG	AGACTCAGAG	5040
124	CCAGTTGGGG	GCGATCTCGG	TGGCCACAG	CTCCAGGCTG	CGCAGCTGGA	CATCGTGCGG	5100
125	GATCAGCCCG	GAGTACTGGC	ACTGGAGCAG	ATACTCCGGA	TCGTGCCGCT	CCACCAGCTT	5160
126	CTCGATCATG	CGGTTGATGT	CGTCCGGGGT	GCCGACCCAC	TCCAGCCCCC	GGTCGACCAG	5220
127	GGTCTGTAG	TCCGAGCCGA	TCGGACCCGT	CTCGCCGGTC	GCGCGCAGCG	CCTCGGTGAA	5280
128	GCCCATGGGG	CCGAACCAGT	TCTCGAAGAT	GAAGCCGCGG	CCGCGGGACG	CCCAGTGGTG	5340
129	GGCCTCGCCG	GAGTCCCGGG	AGACCAGGAC	GTCTTTCATC	ACCCCGACCC	GCTCGCCCCG	5400
130	CCGACGGGTG	CCGTGGCCCC	CGCCCTCGGC	CTCCTCCCGG	TAGATGTCCA	TCAGCCGGGC	5460
131	GACGATCTGG	TCGTGCGGTG	TCATCAGGAT	CGGCACCACG	CCCTCCCGGG	CACAGAACCG	5520
132	GAACGTGTCC	TCACTGAAGC	TGAACGGCTG	GAAGACGGGC	GGGTGGGGGC	GCTGGTAGGG	5580
133	CTTGGGCGCG	ATGCCACCT	CGCGGATGAC	GCCGTTCTCG	TCGAGGCCCC	GGCCGTAGCG	5640
134	GCGCACCGCC	TCGTAGGGGA	ACTCCAGGTC	CGGCACCGGG	ATCGTCCACT	GCTCCCCGGA	5700
135	GTGGGTGAAC	GTCTCGGTG	TCCACGCCCT	CTTGATGATC	TCCCAGTGCT	CCTCGAAGAG	5760
136	GGCAGATTG	CGCCGTCCC	GCTCCCGGCG	GTCCGACAGG	GTGCCGCCGA	CCCCGTACAC	5820
137	CTGCCCCATG	ATGTCGGCCC	AGCGTTCTTG	GAACCCGCGC	GCGATCCCGA	CGAAGGCGCG	5880
138	GCCCCGGGTC	ATGTGGTTCG	GCATCGCCAG	ATCCTCGGCC	AGCCGCAGCG	GATTGTGCAG	5940
139	CGGACGAGC	TTGGCCATCT	GGCCGACCCG	GATGTGCCGG	GTCTGCATGC	CGAGGTAGAG	6000
140	CCCACGATG	ATCGGGTTGT	TGGAGACCTC	GAAACCCTCG	GTGTGGAAGT	GGTGCTCGGT	6060

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141   GAAGGACAGT CCCAGTAGC CGAGTTCGTC GGCCGCCTGC GCCTGCCGGG TGAGCTGCCG 6120
142   GAGCATGTTC TGGTAGTTCT GCGGATTGAC CCCC GCCATA CCCC GCTGGA CCTGCGCATG 6180
143   ACTGCCGACC GTTGGCAGAT AGAAGAGAAT GGACTTCACC CTGGCTCCTC CGGTTCGCGG 6240
144   CGCCCTCCAT TGACGTGCGC CGAAAGCGGC TCGACCGTCC CACTCCGCCC TTGAGTTCCG 6300
145   TCTGACGCCG CGCCAGTCGG CGGGCCGTCC GCCGGGGTGC CCGCCGGGGT CCGCACCCGC 6360
146   CGGACGGCAC GCGCGGCACC GCGCGCGCGG CGCTTCGGGG CACCGGGCTC GACGGGGTGC 6420
147   TCAGCGGGAC GTCCAACGGA AGGCAAGCCC CCGTACCCAG CCTGGTCAAG GCGCTCATCG 6480
148   CCATTCCCTG AGGAGGTCCC GCCTTGACCA CAGCAATCTC CGCGTCCCG ACCGTGCCCCG 6540
149   GCTCCGGA CTG GACTG GACCGTGCCA CCCTCATCCA CCCCACCCTC TCCGGAAACA 6600
150   CCGCGGAACG GATCGTGCTG ACCTCGGGTG CCGGCAGCCG GGTCCGCGAC ACCGACGGCC 6660
151   GGGAGTACCT GGACGCGAGC GCGCTCCTCG GGGTGACCCA GGTGGGGCCG GCGCGGGCCG 6720
152   AGCTGGCCCG GGTGCGGGCC GAGCAGATGG CCCGGCTGGA GTACTTCCAC ACCTGGGGGA 6780
153   CGATCAGCAA CGACCGGGCG GTGGAGCTGG CCGCACGGCT GGTGGGGCTG AGCCCGGAGC 6840
154   CGCTGACCCG CGTCTACTTC ACCAGCGGCG GGGCCGAGGG CAACGAGATC GCCCTGCGGA 6900
155   TGGCCCGGCT CTACCACCAC CGGCGCGGGG AGTCCGCCCG TACCTGGATA CTCTCCCGCC 6960
156   GGTGCGCCTA CCACGGCGTC GGATACGGCA GCGGCGGCGT CACCGGCTTC CCCGCTACC 7020
157   ACCAGGGCTT CGGCCCTCC CTCCCGGACG TCGACTTCCT GACCCCGCCG CAGCCCTACC 7080
158   GCCGGGAGCT GTTCGCGGT TCCGACGTCA CCGACTTCTG CCTCGCCGAA GTCGCGGAGA 7140
159   CCATCGACCG GATCGGCCCC GAGCGGATCG CGGCGATGAT CGGCGAGCCG ATC 7193

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161 (2) INFORMATION FOR SEQ ID NO: 2:

162 (i) SEQUENCE CHARACTERISTICS:

163 (A) LENGTH: 145 base pairs

164 (B) TYPE: nucleic acid

165 (C) STRANDEDNESS: single

166 (D) TOPOLOGY: linear

167 (ii) MOLECULE TYPE: Other

168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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169   GTGACCCGGC CTCGGGCTT TCCGCGCAC ACCCAGGGT CCGTGTCGGG GAGTCTGCTG 60
170   CGCCGGGTGG CGGGCCACTA TCCACCGGG GTGGTCTTGG TCACCGGTCC GGCCGAGGCT 120
171   CCGGGGACGC CGCCGCCCG CATGG 145

```

173 (2) INFORMATION FOR SEQ ID NO: 3:

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 453 base pairs

176 (B) TYPE: nucleic acid

177 (C) STRANDEDNESS: single

178 (D) TOPOLOGY: linear

179 (ii) MOLECULE TYPE: Other

180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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181   ATGTCCTGG CATCGGCCG TATGACGGC GAGCAGCGCA AGGCGGTCAT CACCGCGTAC 60
182   TTCAAGGCGT TCGACAACGG CGGCGTCGGC AGCAGCGCA CCCC GCGAT CGACTACTTC 120
183   GCCGAGGACG CGGTCTTCTT CTTCCTCAAG TGGGGTCTGG CCCGGGGCAA GTCCGAGATC 180
184   GCCCGGCTCT TCGACGACCT CGGGGGCACC ATCCGCTCGA TCACCCACCA TCTGTGGTCC 240
185   GTCAACTGGA TTCTGACCGG GACCGAATC CTCGCCGCGG AGGGCACCAC CCACGGTGAG 300
186   CACCGGGACG GGCGTGCGG GCGGGGTGAC CCCGAGTGG CCGCCGGGCG CTGGTGACG 360
187   GTCTACGAGG TGCGGGACTT CCTCGTCCAC CGGGCCTTCG TCTATCTGGA CCCCATTAC 420
188   GCGGGCAAGG ACACCGCGCG TTACCCGTGG CTG 453

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190 (2) INFORMATION FOR SEQ ID NO: 4:

191 (i) SEQUENCE CHARACTERISTICS:

192 (A) LENGTH: 1032 base pairs

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193      (B) TYPE: nucleic acid
194      (C) STRANDEDNESS: single
195      (D) TOPOLOGY: linear
196  (ii) MOLECULE TYPE: Other
197  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
198      ATGTCCCCTCTCCGCCCCGACGTTCCCGTGTCCGCGTCCG      60
199      CCGGTCCGCG CCCTGCGGGA CTTTCCGCTC AGTGCCAGG GGCTCGGCTG CCTGCCGACC      120
200      ACCGACTTCT ACAGACGCCC GGACCGCGCC CGGGCGACGG CCACATCCG CGCCGCGCTC      180
201      GACGCCGGGG TCACCTGCTT GGACACGCCC GACGTCCAGG GGCTCGGCGC CCGTGAGGAG      240
202      CTGCTCGGAC GGGCGGTGCG GGGCCGCGCG GACGAGGTGC TGATCGCCAC CAAGTTCGCG      300
203      ATGGTGCCTG CGTCCGACGG CGCCTCCAGG GGCTTGTGCG GCGAGCCGTC CTACGTCCGC      360
204      GCGGCCTGCG AACGGTCCCT GCGTCGTCTC GGCACCGACC GCATCGACCT GTACTACCAG      420
205      CACTGGACGG ACCCGGCGGT GCCGATCGAG GAGACCGTGG GTGCGGTGGC CGAGCTGGTG      480
206      CGCGAGGGCA AGGTCCGAGG GTCGCGTCTC TCCGAGCCCT CCGCGGCCAC GCTGCGCCGG      540
207      GCGGACGCGG TGCACCCGCT GACGGCGGTG CAGAGCGAGT GGAGCCTGTG GTCGCGCGGG      600
208      ATCGAGGACG AGGTGGTGCC CGTCTGCCGG GAGCTGGGGA TCGGGATCGT CGCTTACGCC      660
209      CCTCTGGGAC GGGGTTTTCT CACCGGCACC ATCCGCACCA CCGACGATCT GGGGGACGAG      720
210      GACTTCCGCG GGGGCCAGCC CCGGTTTCAG GCTCCGCGCC TCGCGCGCAA CCGCTCGTTG      780
211      CTGCACCGGC TCGCGCCGCT CGCGGACGCT CTGGGGCTGA CCCTGGCACA GCTCGCGCTC      840
212      GCCTGGCTGC ACCACCGGGG CGAGGACGTC GTCCCGATCC CGGGCACCGC GAACCCGGCC      900
213      CATCTCGCGG ACAATCTCGC CGCCGCTCG ATCCGGCTGG ACGACCGGTC CCTCGCGGAG      960
214      GTGACGGCGG CGATCTCCCA CCCGGTGTCC GGGGAGCGGT ACACCCCGGC ATTGCTCGCC      1020
215      ATGATCGGCA AC                                     1032
217  (2) INFORMATION FOR SEQ ID NO: 5:
218      (i) SEQUENCE CHARACTERISTICS:
219          (A) LENGTH: 984 base pairs
220          (B) TYPE: nucleic acid
221          (C) STRANDEDNESS: single
222          (D) TOPOLOGY: linear
223      (ii) MOLECULE TYPE: Other
224      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
225      GTGGAATGCC GCATATTCGA GATCGACGAA CTGCCGTTGC TGGACGGGGA GGTCTGCGG      60
226      GACGCCCGGA TCGGTTACGC CATGTACGGC ACGCCGAACG CCGACGGGAC GAACGTGGTG      120
227      CTCTGTCCGT CGTTCTTCGG CCGGGACCAC ACCGGGTACG ACTGGCTGAT CGGTGCGGGG      180
228      CTGCCGCTGG ACACCCGGCG GTACTGCGTC GTCACCGCCG GACTCTTCGG CAACGGGGTC      240
229      TCCAGCTCGC CCGGCAACCA CCCGTCGGGG TCCCGCTTTC CGCTGATCAC TCCGCAGGAC      300
230      AATGTCGCGG CGCAGCACCG GCTGCTCACC GAGGAGCTGG GGGTACGGGA ACTGGCCCTG      360
231      GTCACGGGCT GGTCGATGGG CGCGGCCAC GCCTACCACT GGGCCGTGTC GCATCCGGGG      420
232      ATGGTGCGCC GGATCGCCCC GATCTGCGGG GCGCCGTTGA GCAGCCCGCA CAGCCTGGTC      480
233      CTGCTGTCCG GTCTGGCCGC GCGCTCAGC GCGGACGCGG GGGAGCGGGG GCGGAAGGCG      540
234      GCGGGCCGGG TGTTCCGCGG GTGGGGGACC TCGCGTTCCT TCTGGGCCCG CCGTGCCAC      600
235      CCGGAGCTGG GTTTCGCCAC CCGCGAGGAG TACCTACCG GCTTCTGGGA GCAGGTCTTC      660
236      CTCTCCGGGC CCGGCGCCGC GGATCTGCTC ACCATGGTGC GCACCTGGGA GAACACGGAT      720
237      GTGGGGGCGA CACCCGGGGC CGGGGGGAGC GTCGAGGCGG CGCTGGCCTC CGTCACGGCG      780
238      CCGGCCCTGG TGCTGCCGGG CGCCCTGGAC GTGTGTTTCG CCGTCGAGGA CGAGAAGCGG      840
239      GTGGCCGATC TGCTGCCGTA TGCCTCGCTG GAGGTGATCC CGGGAGTGTG GGGGCATCTC      900
240      GCGGGGTCCG GGGGGTCCGC CGCCGACCGG GAGTTCATCG GGGGCGCGCT GCGGCGGCTG      960
241      CTGGACAGCC CCGTGGACGG GGGC                                     984
243  (2) INFORMATION FOR SEQ ID NO: 6:

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/071,338

DATE: 03/19/2002
TIME: 18:47:51

Input Set : N:\Crf3\02272002\J071338.raw
Output Set: N:\CRF3\03192002\J071338.raw

L:18 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:19 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]



OIFE

RAW SEQUENCE LISTING DATE: 03/19/2002
 PATENT APPLICATION: US/10/071,338 TIME: 17:52:50

Input Set : N:\Cr3\02272002\J071338.raw
 Output Set: N:\CRF3\03192002\J071338.raw

Does Not Comply
 Corrected Diskette Needed

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
 2 (i) APPLICANT: SmithKline Beecham plc et al
 3 (ii) TITLE OF INVENTION: Novel compounds
 4 (iii) NUMBER OF SEQUENCES: 19
 5 (iv) CORRESPONDENCE ADDRESS:
 6 (A) ADDRESSEE: SmithKline Beecham
 7 (B) STREET: Two, New Horizons Court, Great West Road
 8 (C) CITY: Brentford
 9 (D) STATE:
 10 (E) COUNTRY: UK
 11 (F) ZIP: TW8 9EP
 12 (v) COMPUTER READABLE FORM:
 13 (A) MEDIUM TYPE: Diskette
 14 (B) COMPUTER: IBM Compatible
 15 (C) OPERATING SYSTEM: DOS
 16 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 17 (vi) CURRENT APPLICATION DATA:
 C--> 18 (A) APPLICATION NUMBER: US/10/071,338
 C--> 19 (B) FILING DATE: 08-Feb-2002
 20 (C) CLASSIFICATION:
 21 (vii) PRIOR APPLICATION DATA:
 22 (A) APPLICATION NUMBER:
 23 (B) FILING DATE:
 24 (viii) ATTORNEY/AGENT INFORMATION:
 25 (A) NAME: Valentine, Jill B
 26 (B) REGISTRATION NUMBER:
 27 (C) REFERENCE/DOCKET NUMBER: P31731
 28 (ix) TELECOMMUNICATION INFORMATION:
 29 (A) TELEPHONE: 0181-9752000
 30 (B) TELEFAX: 0181-9756294
 31 (C) TELEX:

ERRORED SEQUENCES

602 (2) INFORMATION FOR SEQ ID NO: 19:
 603 (i) SEQUENCE CHARACTERISTICS:
 604 (A) LENGTH: 324 amino acids
 605 (B) TYPE: amino acid
 606 (C) STRANDEDNESS: single
 607 (D) TOPOLOGY: linear
 608 (ii) MOLECULE TYPE: protein

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/071,338

DATE: 03/19/2002
TIME: 17:52:50

Input Set : N:\Crf3\02272002\J071338.raw
Output Set: N:\CRF3\03192002\J071338.raw

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

609	Met	Thr	Ser	Val	Asp	Cys	Thr	Ala	Tyr	Gly	Pro	Glu	Leu	Arg	Ala	Leu
610																15
611	1					5				10						
612	Ala	Ala	Arg	Leu	Pro	Arg	Thr	Pro	Arg	Ala	Asp	Leu	Tyr	Ala	Phe	Leu
613				20					25						30	
614	Asp	Ala	Ala	His	Thr	Ala	Ala	Ala	Ser	Leu	Pro	Gly	Ala	Leu	Ala	Thr
615			35					40					45			
616	Ala	Leu	Asp	Thr	Phe	Asn	Ala	Glu	Gly	Ser	Glu	Asp	Gly	His	Leu	Leu
617		50					55					60				
618	Leu	Arg	Gly	Leu	Pro	Val	Glu	Ala	Asp	Ala	Asp	Leu	Pro	Thr	Thr	Pro
619						70					75					80
620	Ser	Ser	Thr	Pro	Ala	Pro	Glu	Asp	Arg	Ser	Leu	Leu	Thr	Met	Glu	Ala
621						85				90						95
622	Met	Leu	Gly	Leu	Val	Gly	Arg	Arg	Leu	Gly	Leu	His	Thr	Gly	Tyr	Arg
623				100					105						110	
624	Glu	Leu	Arg	Ser	Gly	Thr	Val	Tyr	His	Asp	Val	Tyr	Pro	Ser	Pro	Gly
625			115					120					125			
626	Ala	His	His	Leu	Ser	Ser	Glu	Thr	Ser	Glu	Thr	Leu	Leu	Glu	Phe	His
627		130					135					140				
628	Thr	Glu	Met	Ala	Tyr	His	Arg	Leu	Gln	Pro	Asn	Tyr	Val	Met	Leu	Ala
629		145				150					155					160
630	Cys	Ser	Arg	Ala	Asp	His	Glu	Arg	Thr	Ala	Ala	Thr	Leu	Val	Ala	Ser
631					165					170						175
632	Val	Arg	Lys	Ala	Leu	Pro	Leu	Leu	Asp	Glu	Arg	Thr	Arg	Ala	Arg	Leu
633				180					185				190			
634	Leu	Asp	Arg	Arg	Met	Pro	Cys	Cys	Val	Asp	Val	Ala	Phe	Arg	Gly	Gly
635			195				200					205				
636	Val	Asp	Asp	Pro	Gly	Ala	Ile	Ala	Gln	Val	Lys	Pro	Leu	Tyr	Gly	Asp
637		210				215						220				
638	Ala	Asp	Asp	Pro	Phe	Leu	Gly	Tyr	Asp	Arg	Glu	Leu	Leu	Ala	Pro	Glu
639		225				230					235					240
640	Asp	Pro	Ala	Asp	Lys	Glu	Ala	Val	Ala	Ala	Leu	Ser	Lys	Ala	Leu	Asp
641					245					250						255
642	Glu	Val	Thr	Glu	Ala	Val	Tyr	Leu	Glu	Pro	Gly	Asp	Leu	Leu	Ile	Val
643			260						265					270		
644	Asp	Asn	Phe	Arg	Thr	Thr	His	Ala	Arg	Thr	Pro	Phe	Ser	Pro	Arg	Trp
645			275				280						285			
646	Asp	Gly	Lys	Asp	Arg	Trp	Leu	His	Arg	Val	Tyr	Ile	Arg	Thr	Asp	Arg
647		290					295					300				
648	Asn	Gly	Gln	Leu	Ser	Gly	Gly	Glu	Arg	Ala	Gly	Asp	Val	Val	Ala	Phe
649		305				310					315					320
650	Thr	Pro	Arg	Gly												
651	Attorney Docket : P31731 - 19 -															
652	Group Art Unit: 1652															
Attorney Docket : P31731	- 1 -															
E--> 653	Group Art Unit: 1652															

delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/071,338

DATE: 03/19/2002

TIME: 17:52:51

Input Set : N:\Crf3\02272002\J071338.raw

Output Set: N:\CRF3\03192002\J071338.raw

L:18 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:19 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:653 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:653 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:653 M:330 E: (2) Invalid Amino Acid Designator, 3
L:653 M:203 E: No. of Seq. differs, LENGTH:Input:324 Found:327 SEQ:19